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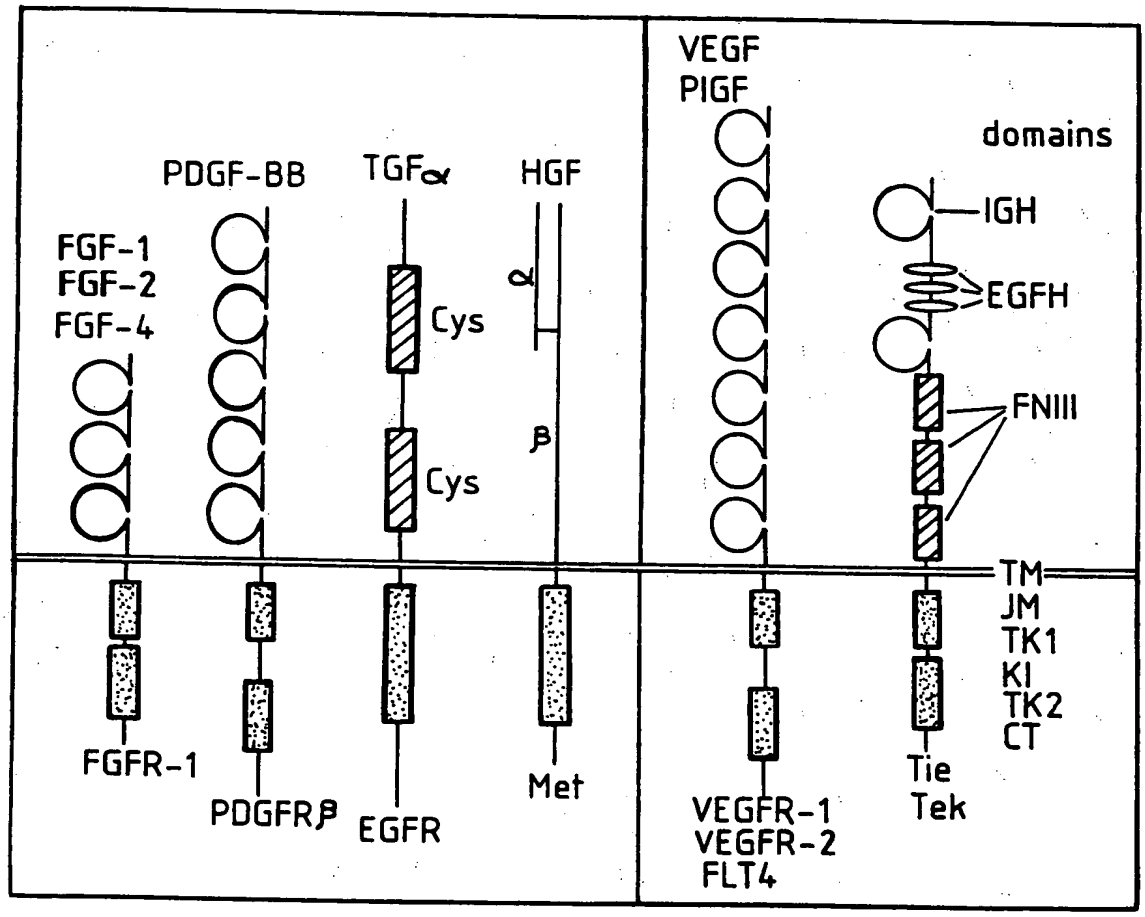


FIG. 1

```
            1                                                    50
PDGF-A      .......... .......... .......... .......... .MRTLACLLL
PDGF-B      .......... .......... .......... .......... MNRCWA.LFL
PlGF-1      .......... .......... .......... .......... ..........
VEGF165     .......... .......... .......... .......... ..........
VEGF-B167   .......... .......... .......... .......... ..........
VEGF-C      MHLLGFFSVA CSLLAAALLP GPREAPAAAA AFESGLDLSD AEPDAGEATA

            51                                                   100
PDGF-A      LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE IDSVGSEDSL
PDGF-B      SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH GDP.GEEDGA
PlGF-1      .......... ......MPVM RLFPC..FLQ LLAGLAL... PAVPPQQW..
VEGF165     .......... .........M NFLLS..WVH WSLALLLYLH HAKWSQAA..
VEGF-B167   .......... .........M SPLLR..RLL LAALLQLAPA QAPVSQP...
VEGF-C      YASKDLEEQL RSVSSVDELM TVLYPEYWKM YKCQLRKGGW QHNREQANLN

            101                                                  150
PDGF-A      DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP AVCKTRTVIY
PDGF-B      ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI AECKTRTEVF
PlGF-1      .....ALSAG NGSSEVEVVP FQE.VWGR.. .......... SYCRALERLV
VEGF165     .....PMAEG GGQNHHEVVK FMD.VYQR.. .......... SYCHPIETLV
VEGF-B167   .........D APGHQRKVVS WID.VYTR.. .......... ATCQPREVVV
VEGF-C      SRTEETIKFA AAHYNTEILK SIDNEWRK.. .......... TQCMPREVCI

            151                                                  200
PDGF-A      EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS RVHHRSVKVA
PDGF-B      EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT QVQLRPVQVR
PlGF-1      DVVSEYPSEV ..EHMFSPSC VSLLRCTGCC GDENLHCVPV ETANVTMQLL
VEGF165     DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT EESNITMQIM
VEGF-B167   PLTVELMGTV ..AKQLVPSC VTVQRCGGCC PDDGLECVPT GQHQVRMQIL
VEGF-C      DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT STSYLSKTLF
```

FIG. 2A

```
     201                                                                  250
PDGF-A   KVEYVRKKPK LKEVQVRLEE HLECACAT.. .......... TSLNPDYREE
PDGF-B   KIEIVRKKPI FKKATVTLED HLACKCETVA AARPVTRSPG GSQEQRAKTP
PlGF-1   KIRSG..DRP .SYVELTFSQ HVRCECRPLR EK........ ..........
VEGF165  RIKPH..QGQ .HIGEMSFLQ HNKCECRPKK DR........ ..........
VEGF-B167 MIRYP..SSQ ..LGEMSLEE HSQCECRPKK KD........ ..........
VEGF-C   EITVPLSQGP .KPVTISFAN HTSCRCMSKL DVYRQVHSII RRSLPATLPQ

     251                                                                  300
PDGF-A   DTDVR..... .......... .......... .......... ..........
PDGF-B   QTRVTIRTVR VRRPPKGKHR KFKHTHDKTA LKETLGA... ..........
PlGF-1   .......... .......... .......... .MKPERCGDA VPRR......
VEGF165  .......... .......... .......... .ARQENPCGP CSERRKHLFV
VEGF-B167 .......... .......... .........S AVKPDSPRPL CPRCTQHHQR
VEGF-C   CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG FHDICGPNKE

     301                                                                  350
PDGF-A   .......... .......... .......... .......... ..........
PDGF-B   .......... .......... .......... .......... ..........
PlGF-1   .......... .......... .......... .......... ..........
VEGF165  QDPQTCKCSC KNTDS.RCKA RQLELNERTC RCDKPRR... ..........
VEGF-B167 PDPRTCRCRC RRRSFLRCQG RGLELNPDTC RCRKLRR... ..........
VEGF-C   LDEETCQCVC RAGLRPASCG PHKELDRNSC QCVCKNKLFP SQCGANREFD
```

FIG. 2B

```
            351                                                        400
PDGF-A      .......... .......... .......... .......... ..........
PDGF-B      .......... .......... .......... .......... ..........
PlGF-1      .......... .......... .......... .......... ..........
VEGF165     .......... .......... .......... .......... ..........
VEGF-B167   .......... .......... .......... .......... ..........
VEGF-C      ENTCQCVCKR TCPRNQPLNP GKCACECTES PQKCLLKGKK FHHQTCSCYR

            401                                                434
PDGF-A      .......... .......... .......... ....
PDGF-B      .......... .......... .......... ....
PlGF-1      .......... .......... .......... ....
VEGF165     .......... .......... .......... ....
VEGF-B167   .......... .......... .......... ....
VEGF-C      RPCTNRQKAC EPGFSYSEEV CRCVPSYWKR PQMS
```

FIG. 2C

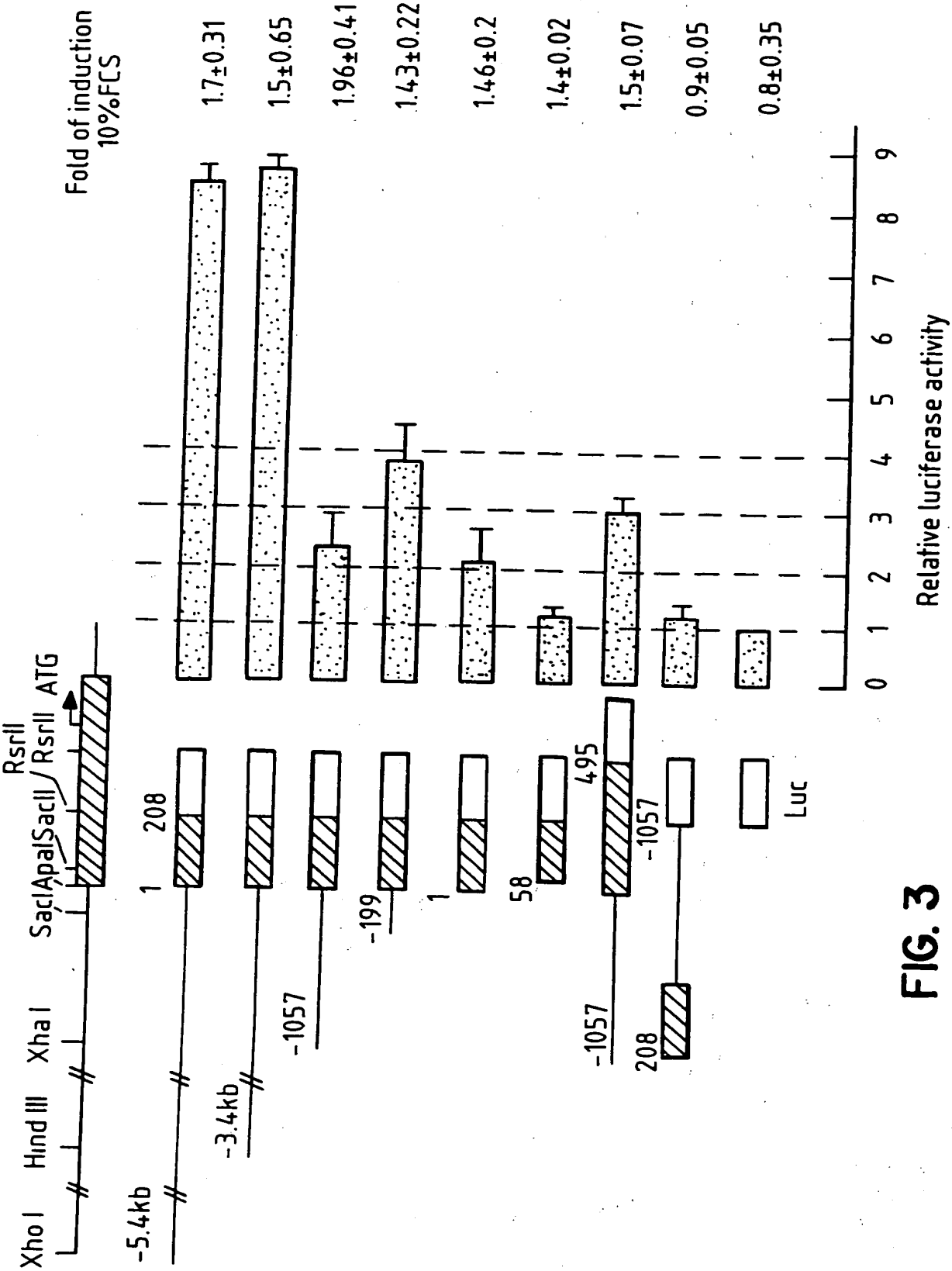


FIG. 3

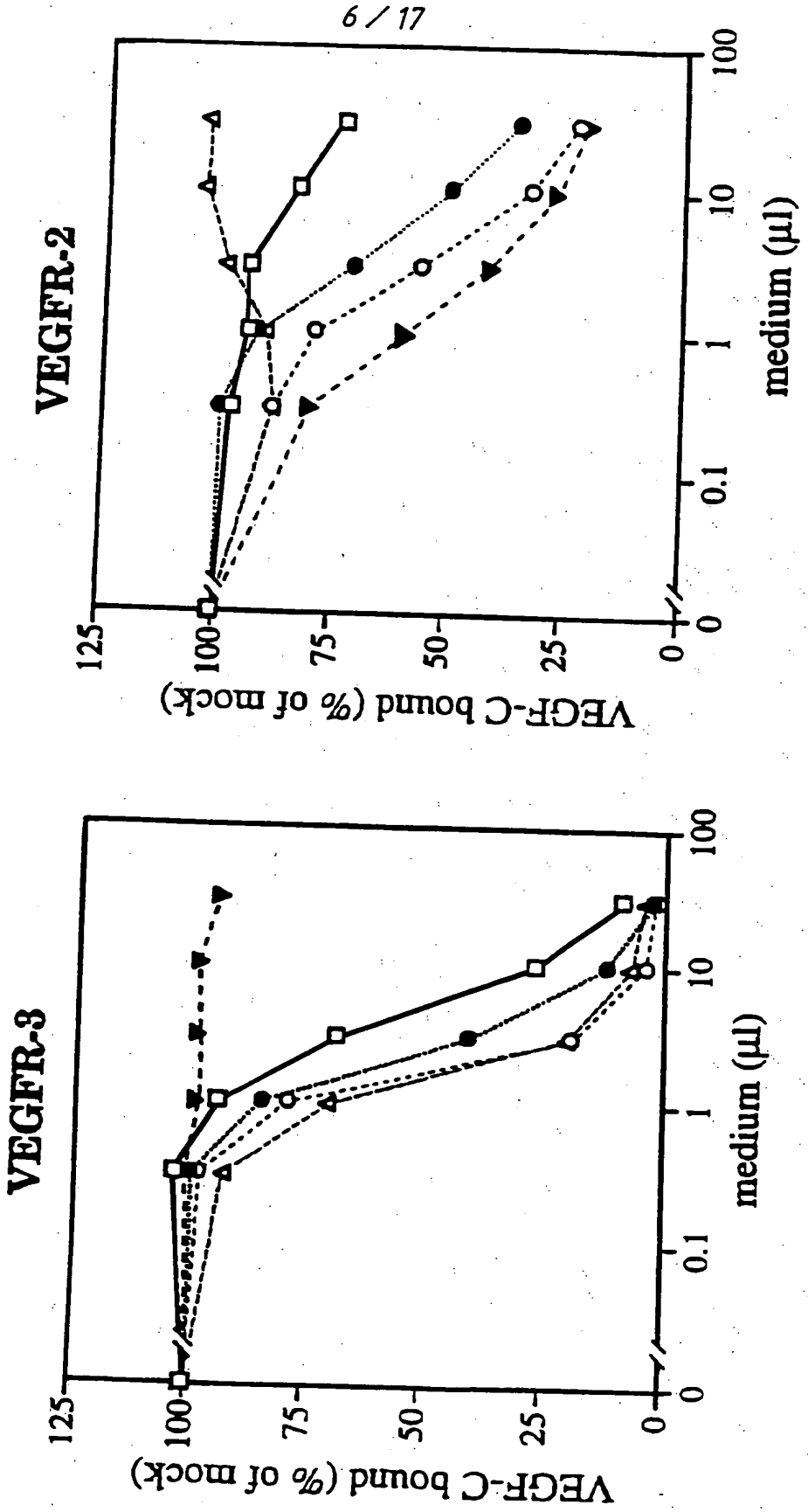


FIG. 4

VEGF-C alignment

```
      1                                                        50
Hum   MMLLGFFSVA CSLLAAALLP GPREAPAAAA AFESGLDLSD AEPDAGEATA
Mou   MHLLCFLSLA CSLLAAALIP SPREAPATVA AFESGLGFSE AEPDGGEVKA
Qua   MHLLEMLSLG CCLAAGAVLL GPRQPPVA.A AYESGHGYYE EEPGAGEPKA

      51                                                      100
Hum   YASKDLEEQL RSVSSVDELM TVLYPEYWKM YKCQLRKGGW QHNREQANLN
Mou   FEGKDLEEQL RSVSSVDELM SVLYPDYWKM YKCQLRKGGW Q....QPTLN
Qua   HASKDLEEQL RSVSSVDELM TVLYPEYWKM FKCQLRKGGW QHNREHSSSD

      101                                                     150
Hum   SRTEETIKFA AAHYNTEILK SIDNEWRKTQ CMPREVCIDV GKEFGVATNT
Mou   TRTGDSVKFA AAHYNTEILK SIDNEWRKTQ CMPREVCIDV GKEFGAATNT
Qua   TRSDDSLKFA AAHYNAEILK SIDTEWRKTQ GMPREVCVDL GKEFGATTNT

      151                                                     200
Hum   FFKPPCVSVY RCGGCCNSEG LQCMNTSTSY LSKTLFEITV PLSQGPKPVT
Mou   FFKPPCVSVY RCGGCCNSEG LQCMNTSTGY LSKTLFEITV PLSQGPKPVT
Qua   FFKPPCVSIY RCGGCCNSEG LQCMNISTNY ISKTLFEITV PLSHGPKPVT

      201                                                     250
Hum   ISFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATLPQCQAAN KTCPTNYMWN
Mou   ISFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATLPQCQAAN KTCPTNYVWN
Qua   VSFANHTSCR CMSKLDVYRQ VHSIIRRSLP ATQTQCHVAN KTCPKNHVWN

      251                                                     300
Hum   NHICRCLAQE DFMFSSDAGD DSTDGFHDIC GPNKELDEET CQCVCRAGLR
Mou   NYMCRCLAQQ DFIFYSNVED DSTNGFHDVC GPNKELDEDT CQCVCKGGLR
Qua   NQICRCLAQH DFGFSSHLGD SDTSEGFHIC GPNKELDEET CQCVCKGGVR

      301                                                     350
Hum   PASCGPHKEL DRNSCQCVCK NKLFPSQCGA NREFDENTCQ CVCKRTCPRN
Mou   PSSCGPHKEL DRDSCQCVCK NKLFPNSCGA NREFDENTCQ CVCKRTCPRN
Qua   PISCGPHKEL DRASCQCMCK NKLLPSSCGP NKEFDEEKCQ CVCKKTCPKH

      351                                                     400
Hum   QPLNPGKCAC ECTESPQKCL LKGKKFHHQT CSCYRRPCTN RQKACEPGFS
Mou   QPLNPGKCAC ECTENTQKCF LKGKKFHHQT CSCYRRPCAN RLKHCDPGLS
Qua   HPLNPAKCIC ECTESPNKCF LKGKRFHHQT CSCYRPPCTV RTKRCDAGFL

      401                 420
Hum   YSEEVCRCVP SYWKRPQMS*
Mou   FSEEVCRCVP SYWKRPHLN.
Qua   LAEEVCRCVR TSWKRPLMN*
```

FIG. 5

Reducing

FIG. 6A

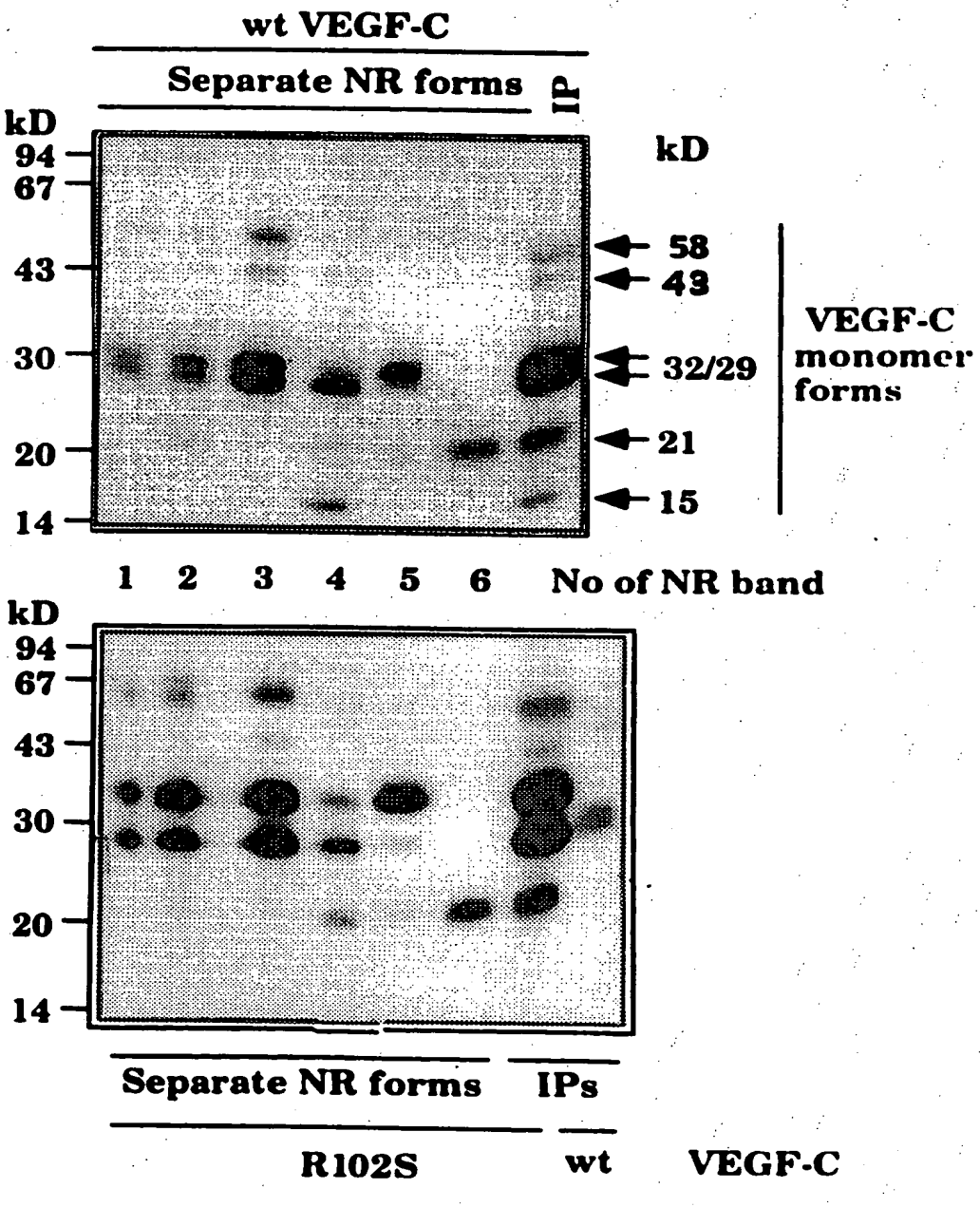


FIG. 6C

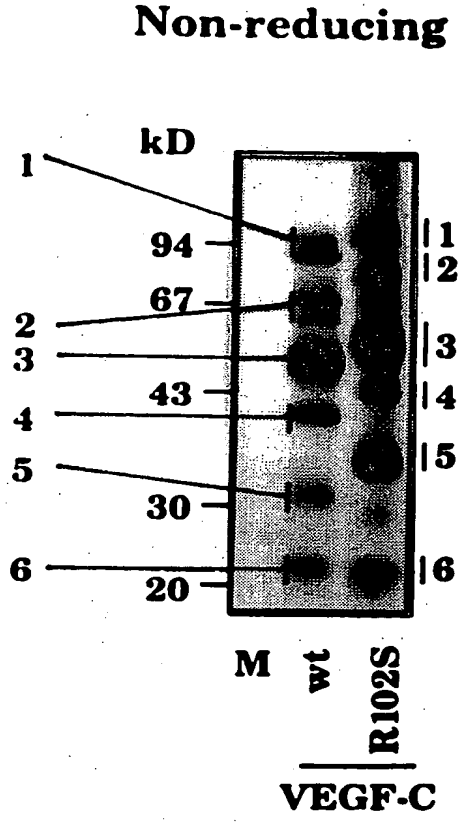
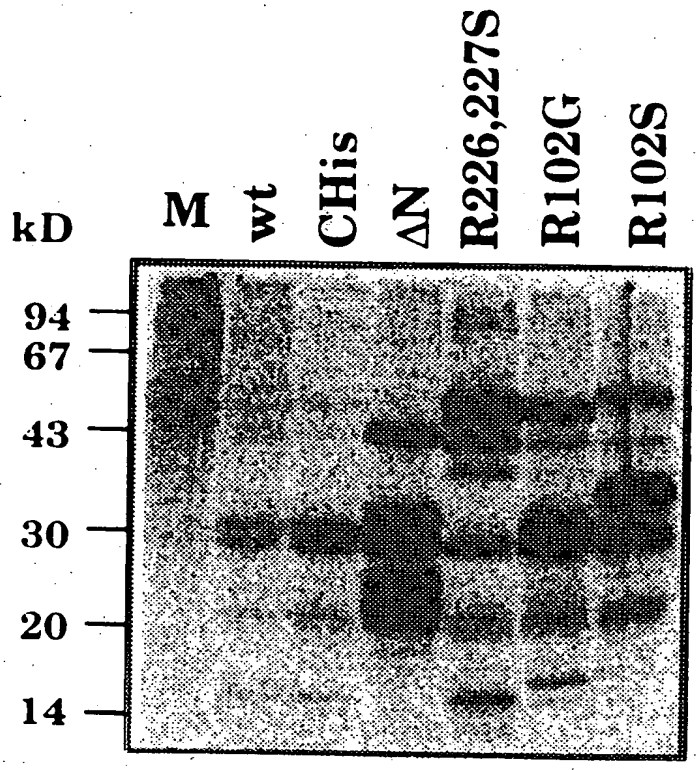


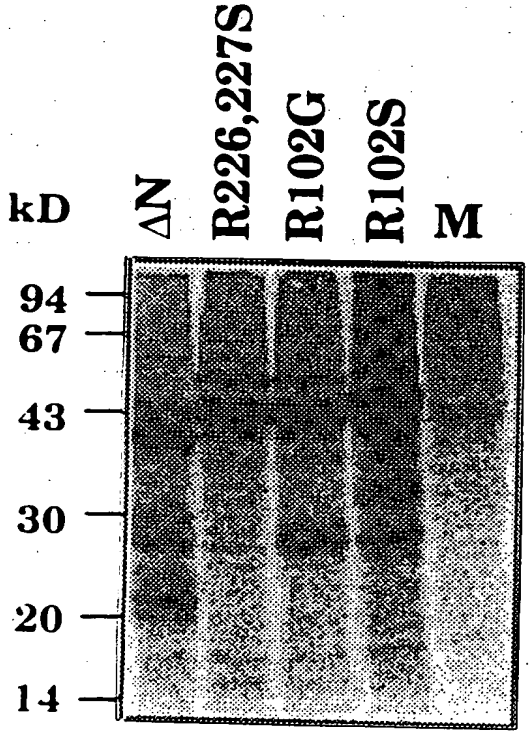
FIG. 6B

FIG. 7A



Media

FIG. 7B



Lysates

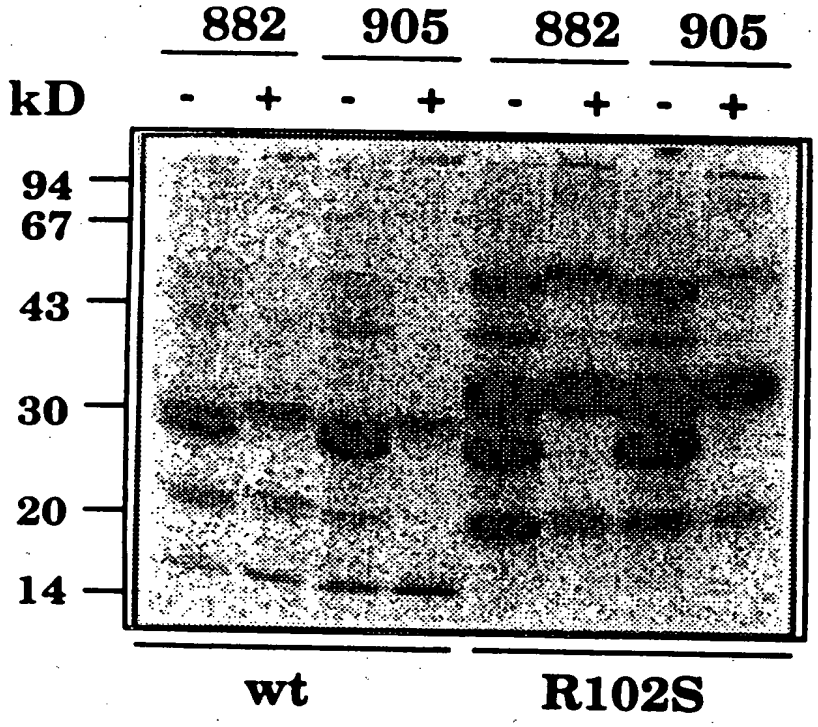


FIG. 8A

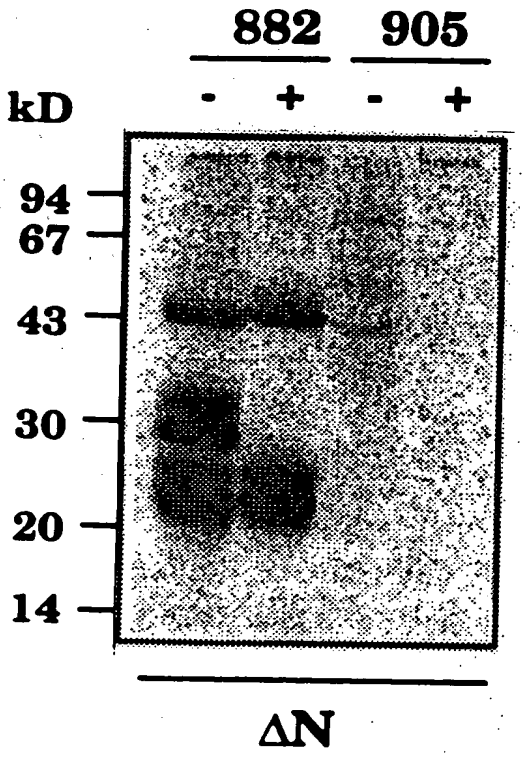


FIG. 8B

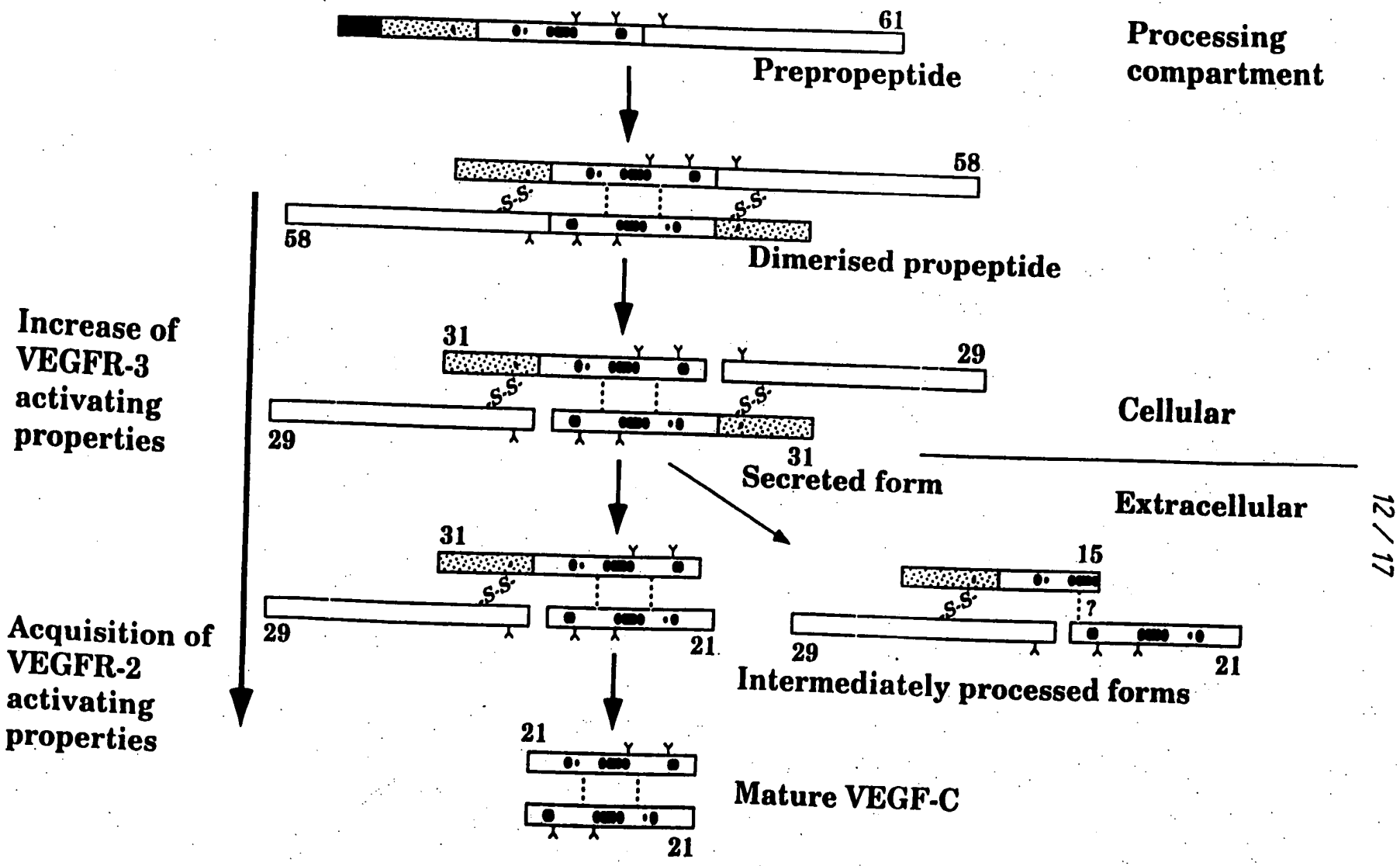


FIG. 9

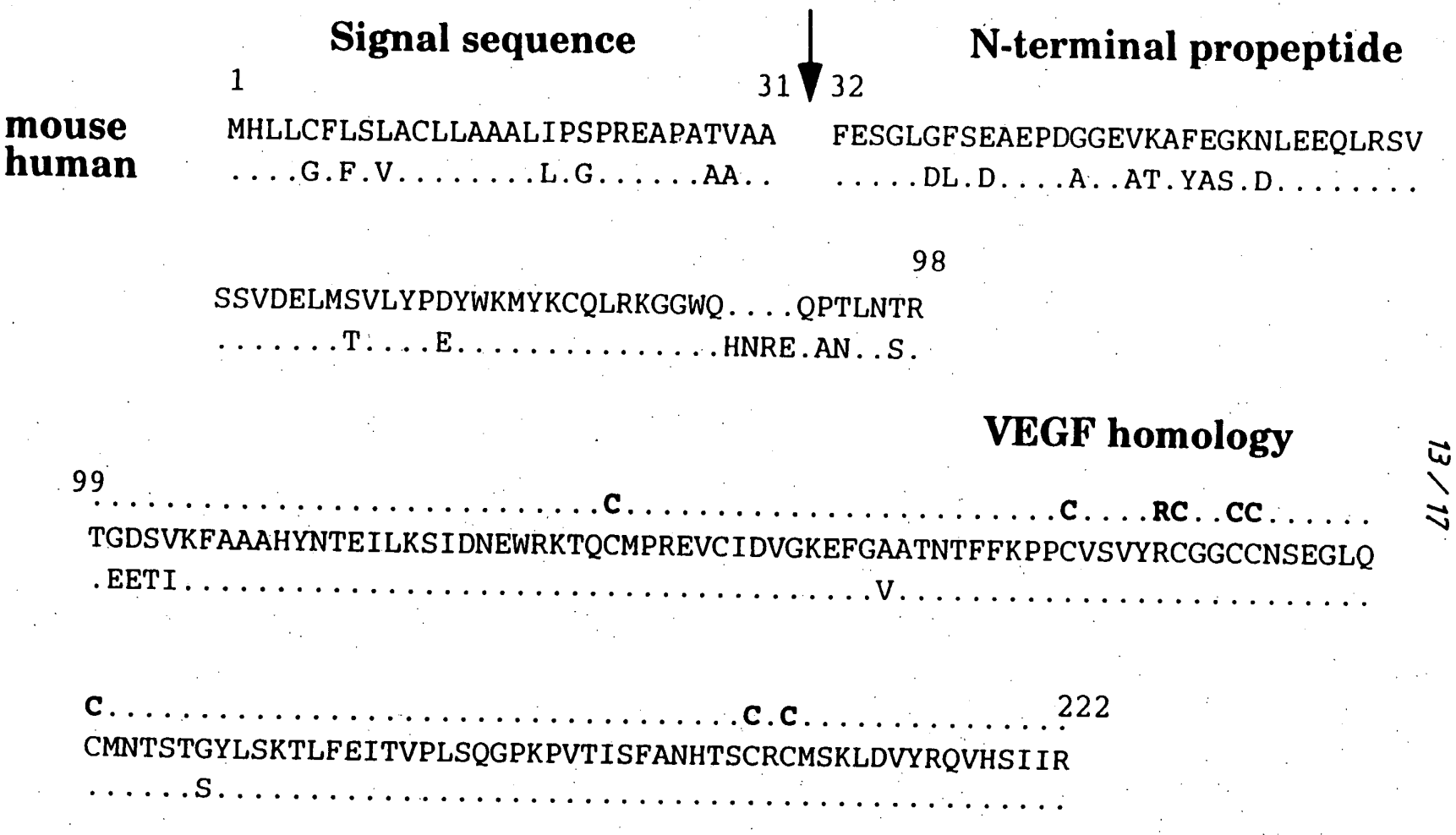


FIG. 10A

BR3P homology

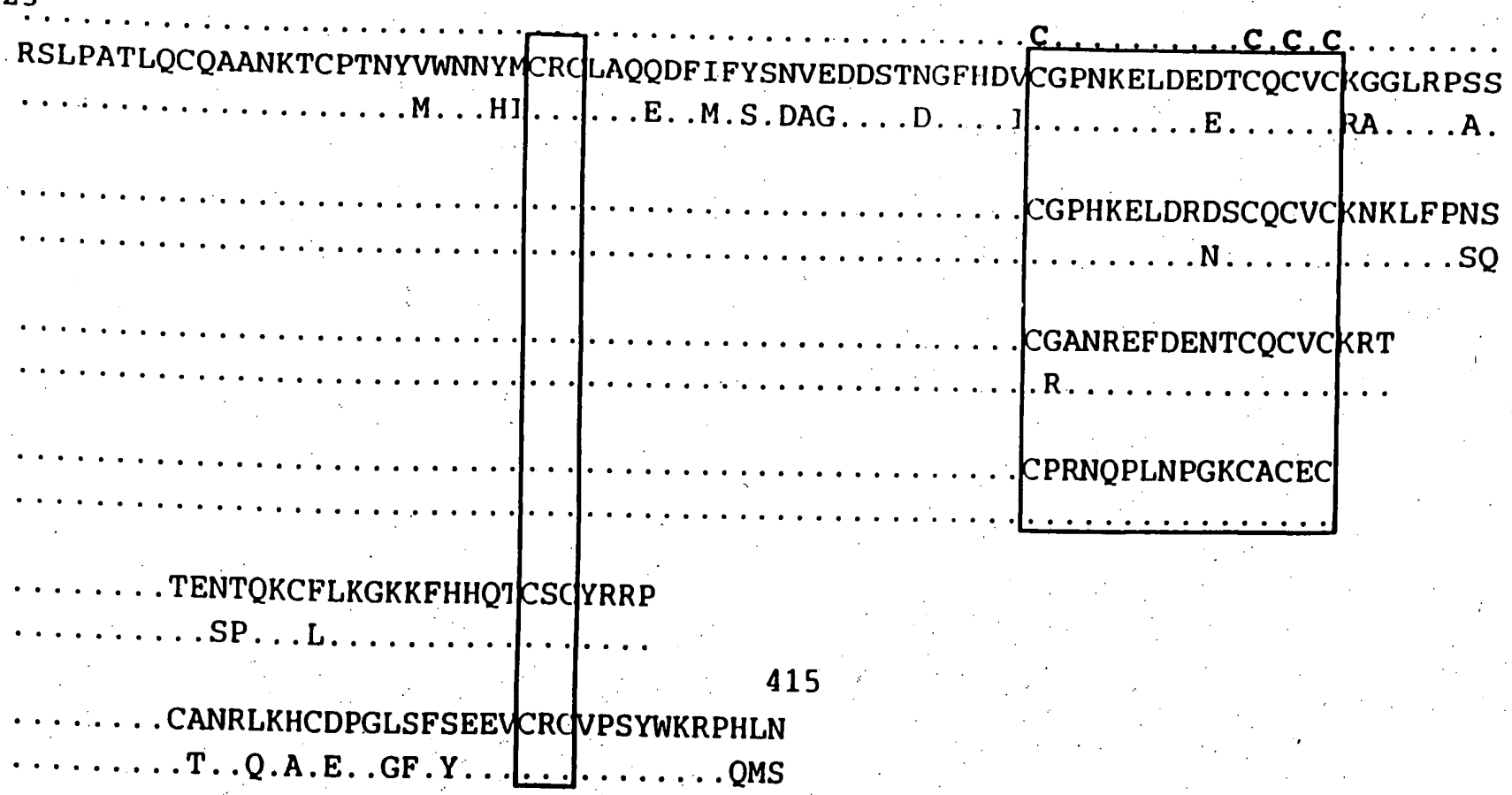


FIG. 10B

HUMAN

Exon length	**Donor site**	**Intron length**	**Acceptor site**
	.....G...E...A...T(49)		
E1	.....GGC.GAG.GCC.ACG.gtaggtctgcgt	>10.kb.	.TTTCTTTGACAG.GCT.TAT.GCA.AGC
	.....E...I...L...K(116)		
E2.214.bp.	.GAG.ATC.TTG.AAA.Agtaagtatggg	.1.6.kb.	...atgacttgacagGT.ATT.GAT.AAT
	.....L...S...K...T(180)		
E3.191.bp.	.CTC.AGC.AAG.ACG.gtgggtattgt	.....9.kb.	ccctttttgtag.TTA.TTT.GAA.ATT
	.....T...L...P...Q(231)		
E4.152.bp.	.ACA.CTA.CCA.CAgtgagtatgaattaaa	.>10.kb.	.ttcttccaaagG.TGT.CAG.GCA.GCG
	.....A...G...D...(266)		
E5.107.bp.	.GCT.GGA.GAT.Ggtagcagaatg	.....301.bp.	...ctatttgtctagAC.TCA.ACA.GAT
	.....Q...T...C...S(378)		
E6.334.bp.	.CAA.ACA.TGC.AGgtaagagatcc	.....>10.kb.	.tgttctcctagC.TGT.TAC.AGA.CGG
	.....Q...M...S(419)Stop.....		
E7.(501).bp.	.CAA.ATG.AGC.TAA.GTATGTACTGTT	...ATTGTATTAT	

FIG. 11A

MOUSE

Exon length	Donor site	Intron length	Acceptor site
	.....G...E...V...K(49)		.....A...F...E...G.
E1	.....GGC.GAG.GTC.AAG.gtaggtgcaagg.	>10.kb.	attgtctttgacag.GCT.TTT.TGA.AGG
	.....E...I...L...K(116)		.....S...I...D...N.
E2	.201.bp..GAG.ATC.CTG.AAA.Agtaagtag.....	4.kb....	tgtgactcgacagGT.ATT.GAT.AAT
	.....L...S...K...T(180)		.....L...F...E...I.
E3	.191.bp..CTC.AGC.AAG.ACG.gtaggtat.....	9.kb..	ttgtcccttgtag.TTG.TTT.GAA.ATT
	.....T...L...P...Q(231)		.....C.....Q...A...A.
E4	.152.bp..ACA.TTA.CCA.CAgtgagtatg.....	10.kb.	gtctccccaaaagG.TGT.CAG.GCA.GCT
	.....N...V...E...D(266)		.....D.....S...T...N.
E5	.107.bp..AAT.GTT.GAA.GAT.Ggtaagtaaaa...	350.bp.....	tctagAC.TCA.ACC.AAT
	.....Q...T...C...S(378)		.....C...Y...R...R.
E6	.334.bp..CAA.ACA.TGC.AGgtaaggagtgt.....	6.kb..	ttttcccctagT.TGT.TAC.AGA.AGA
	.....H...L...N(415)Stop.....		polyA.....
E7	.506.bp..CAT.CTG.AAC.TAA.GATCATACC...		ATTGTATTATAAgctgtgaag

FIG. 11B

Schematic structure of the human VEGF-C gene

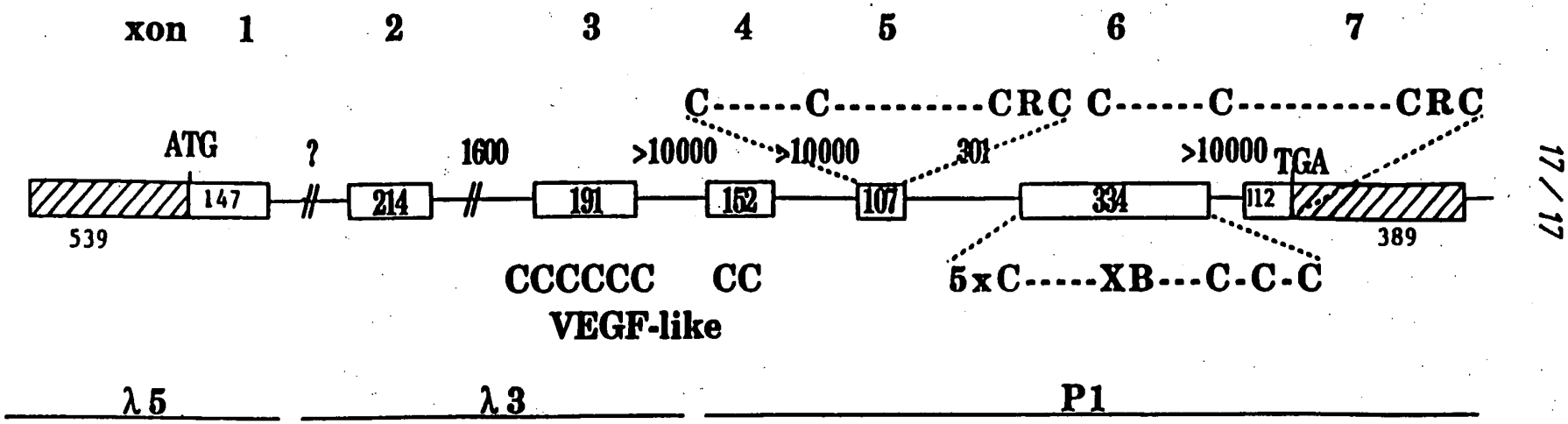


FIG. 12